AMENDMENTS

TO THE SPECIFICATION

Please replace paragraph 16 at page 9 line 19 through page 10 line 21 of the specification with a replacement paragraph amended as follows:

- - According to a preferential embodiment of the invention, the coding sequence of the marker gene is chosen from the coding sequences of a reporter gene, the expression of which is easily measured, in particular GUS (U.S. Pat. No. 5,268,463, U.S. Pat. No. 5,599,670) or GFP (U.S. Pat. No. 5,491,084, U.S. Pat. No. 5,741,668), the coding sequences for a gene for tolerance to an antibiotic or a herbicide, such as the genes for resistance to hygromycin (*hph*: Punt et al., 1987), to phleomycin (*ble*: Drocourt, 1990) or to the herbicide bialaphos (*Bar*: Pall and Brunelli, 1993), or a gene for resistance to sulfonylureas (Sweigard et al., 1997). According to another preferential embodiment of the invention, the marker gene is chosen from the sequences of genes encoding enzymes, which are functional in fungi. Advantageously, the marker gene is the nitrate reductase or nitrilase gene. When the fragment according to the invention is integrated into an nia- fungus, the strain transformed with this construct conserves a mutant phenotype. The appearance of nia+ colonies on a minimum medium ($NaNO_3$ as the only nitrogen source) reveals the excision of the Impala transposon allowing the expression of the *niaD* gene. These nia+ revertants can be selected on this medium due to their dense and aerial phenotype which is different from the low flat phenotype of the nia- colonies. The use of the *niaD* gene as a marker requires the use of an nia- fungus. The methods for identifying nia- fungi are well known to those skilled in the art. Mention will in particular be made of the method described by Daboussi et al. (1989).